

# Model-based Insulin Sensitivity and Pharmacodynamic (PD) Surfaces

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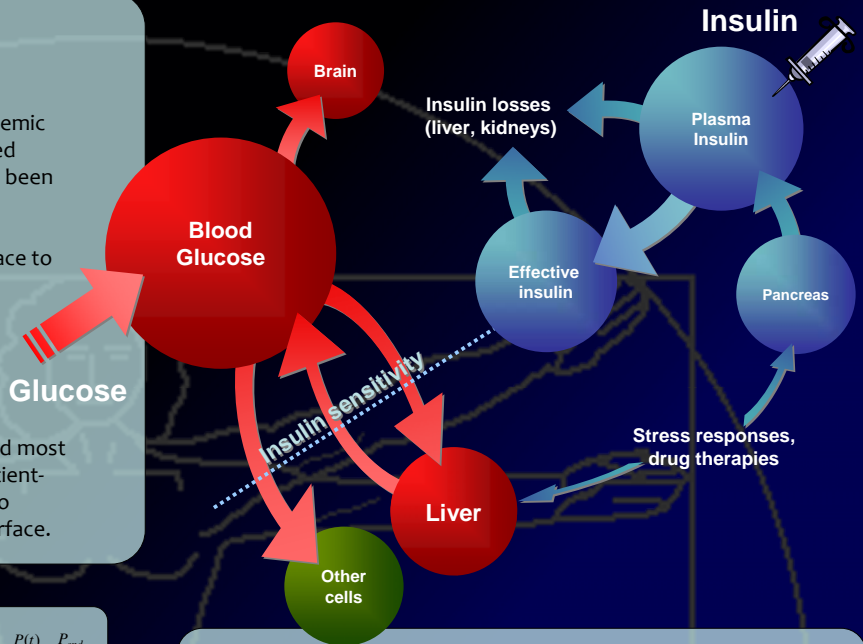
## Background and Aims

The main methods for determining insulin sensitivity with high resolution are either clinical (hyperinsulinemic eu- or hyper-glycemic clamp) or model-based (e.g. FSIVGTT). Typically, the model-based methods use some form of the Minimal Model (MM), which has been shown to underestimate insulin sensitivity in some cases.

This research presents a method of analysing a model's PD surface to determine:

- If its fundamental dynamics capture clinical behaviours
- What, if any, dynamics are missing from a model
- What, if any, dynamics are not necessary

There is currently no fixed method for doing such an analysis and most models are validated on the ability to fit time trajectories of patient-specific clinical data. This approach tests the ability of a model to capture data and trends (in steady state) across an entire PD surface.



	Value
$P_G$	0.006 min <sup>-1</sup>
$V_G$	13.3 L (for 70kg), $V_G = 0.19 \times \text{Mass (kg)}$
$P_{end}$	1.2 mmol/L/min (0 for the MM case)
$S_I$	1.5e-3 - 3.5e-3 L/mU/min
$\alpha_G$	1/20 - 1/80 L/mU (0 for the MM case)
$\alpha_{G2}$	1/5 - 1/20 L/mmol (0 for the MM case)

ND1, 2 and MM:  $\dot{G} = -p_G G - S_I \frac{G}{1 + \alpha_{G2} G} + \frac{Q}{1 + \alpha_G Q} + \frac{P(t)}{V_G} + \frac{P_{end}}{V_G}$

RM:

EndoBal = Hepatic - Renal - P13 - P14

Hepatic =  $-0.46 \text{ min}^{-1} G - 1.475 \text{ mmol/min/mU } I_t + 1.259 \text{ mmol/L/min}$ ;  $G_{max} = 12.0 \text{ mmol/L}$

Renal =  $0.004 \text{ L/mmol/min } G^2 - 0.064 \text{ min}^{-1} G + 0.278 \text{ mmol/L/min}$

P13 =  $0.56 \text{ min}^{-1} \times G / (G + 1.5 \text{ mmol/L})$

P14 =  $5.09 \text{ mmol/L/min/mU } G \times I_t / (G + 5.0 \text{ mmol/L})$

$I_t = I \times 1 / (1 - 0.083 \text{ mU/L})^{1.77} + (0.539 \text{ mU/L})^{1.77} / (1.77)$

System models

## Methodology

Four clinically validated models are analysed:

- Minimal Model (MM)
- A Receptor Model (RM) from Arleth et al (2000)
- Two non-linear dynamic models (ND1 and ND2)

Two sets of euglycemic and hyperglycemic clamp data are used:

- Data Set #1: Eu- and hyper-glycemic clamps are used to find a set of population parameters for each model (N=77)
- Data Set #2: Euglycemic clamp data from a lower insulin sensitivity cohort (N = 146) are used to see if the fitted models from step #1 can fit by just shifting the insulin sensitivity parameter (A model validation test)

Retrospective clamp Data Set #1

Population parameter identification via Grid Search

PD Surfaces compared to clinical data

Retrospective clamp Data Set #2 (lower insulin sens) to test trends

## Results and Conclusions

Performance Metrics:

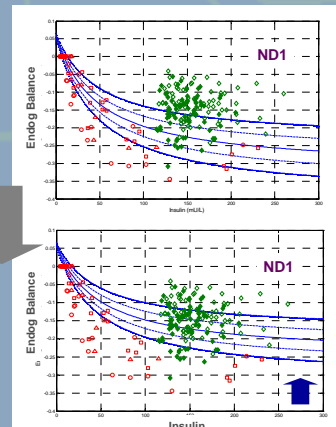
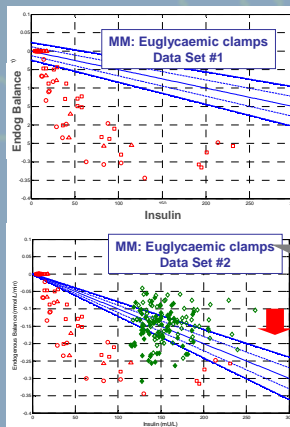
- RMS Error (RMS)
- Absolute Mode of Error (AME)
- Frequency of Error Near Zero (FNZ)

Data Set #1 Results:

Model	Values
ND1	$\alpha_G = 1/47 \text{ L/mU}$ , $\alpha_{G2} = 0 \text{ L/mmol}$ , $S_I = 0.0016 \text{ L/mU/min}$ RMS = 0.07; AME = -0.01, FNZ = 36
ND2	$\alpha_G = 1/47 \text{ L/mU}$ , $\alpha_{G2} = 1/6 \text{ L/mmol}$ , $S_I = 0.0029 \text{ L/mU/min}$ RMS = 0.05; AME = -0.01, FNZ = 39
ND2 Best FNZ	$\alpha_G = 1/50 \text{ L/mU}$ , $\alpha_{G2} = 1/6 \text{ L/mmol}$ , $S_I = 0.0032 \text{ L/mU/min}$ RMS = 0.05; AME = -0.00, FNZ = 38
MM	$\alpha_G = \alpha_{G2} = 0 \text{ L/mU} \& \text{ L/mmol}$ , $S_I = 0.0001 \text{ L/mU/min}$ RMS = 0.29; AME = -0.05, FNZ = 24
RM	RMS = 0.04; AME = -0.01, FNZ = 32

Data Set #2 Results: Scaling Insulin Sensitivity

	RMS	FNZ (of 146)	Scaled $S_I$	Prior $S_I$	$\alpha_{G1}$	$\alpha_{G2}$
MM	0.56	12	2.0e-4	1.0e-4	0	0
ND1	0.05	54	1.3e-3	1.6e-3	1/47	0
ND2	0.05	60	2.3e-3	3.1e-3	1/47	1/6
RM	0.05	61	0.40	1.0	1.77 <sup>th</sup> power or ~1/50	1/5



Note: MM slope high for Data Set #1 to reduce the error for hyperglycemic clamp results not shown here, thus reducing total error

- MM under predicts insulin sensitivity. MM at low insulin sensitivity provides the wrong trend result. These match reported results.

- Saturation dynamics play an important role in providing good fits across PD surface.

- Trend prediction is also reliant on the use of (at least) effective insulin saturation, which the MM does not have.

- Approach can complement typical fitting and prediction validation methods and provide information on which dynamics are necessary or sufficient in any similar model.